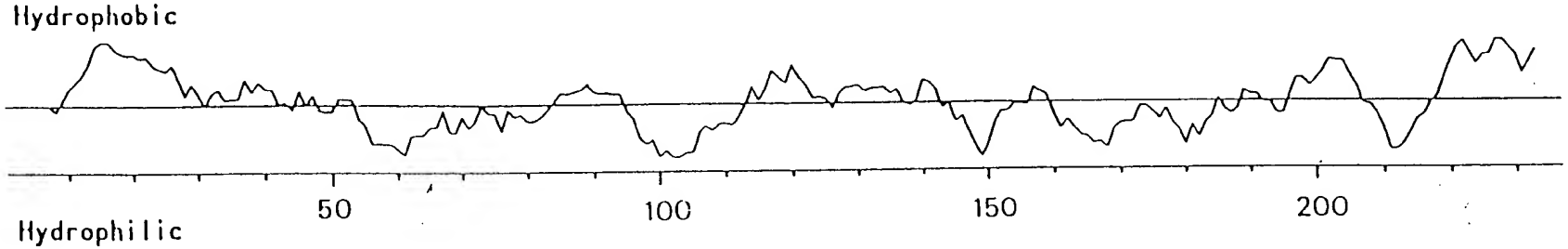
```
  1 AAAGACAAACTGCACCCACTGAACTCCGCAGCTAGCATCCAAATCAGCCCTTGAGATTTGAGGCCTTGGAGACTCAGGAGTTTTGAGAGC

 91 AAAATGACAACACCCAGAAATTCAGTAAATGGGACTTTCCCGGCAGAGCCAATGAAAGGCCCTATTGCTATGCAATCTGGTCCAAAACCA
  1    MetThrThrProArgAsnSerValAsnGlyThrPheProAlaGluProMetLysGlyProIleAlaMetGlnSerGlyProLysPro
                                  ---CHO---

181 CTCTTCAGGAGGATGTCTTCACTGGTGGGCCCCACGCAAAGCTTCTTCATGAGGGAATCTAAGACTTTGGGGGCTGTCCAGATTATGAAT
 30 LeuPheArgArgMetSerSerLeuValGlyProThrGlnSerPhePheMetArgGluSerLysThrLeuGlyAlaValGlnIleMetAsn
                                                                ============================

271 GGGCTCTTCCACATTGCCCTGGGGGGTCTTCTGATGATCCCAGCAGGGATCTATGCACCCATCTGTGTGACTGTGTGGTACCCTCTCTGG
 60 GlyLeuPheHisIleAlaLeuGlyGlyLeuLeuMetIleProAlaGlyIleTyrAlaProIleCysValThrValTrpTyrProLeuTrp
    ================================================================================================

361 GGAGGCATTATGTATATTATTTCCGGATCACTCCTGGCAGCAACGGAGAAAAACTCCAGGAAGTGTTTGGTCAAAGGAAAAATGATAATG
 90 GlyGlyIleMetTyrIleIleSerGlySerLeuLeuAlaAlaThrGluLysAsnSerArgLysCysLeuValLysGlyLysMetIleMet
    ==========================================                                  =========

451 AATTCATTGAGCCTCTTTGCTGCCATTTCTGGAATGATTCTTTCAATCATGGACATACTTAATATTAAAATTTCCCATTTTTTAAAAATG
120 AsnSerLeuSerLeuPheAlaAlaIleSerGlyMetIleLeuSerIleMetAspIleLeuAsnIleLysIleSerHisPheLeuLysMet
    ================================================================

541 GAGAGTCTGAATTTTATTAGAGCTCACACACCATATATTAACATATACAACTGTGAACCAGCTAATCCCTCTGAGAAAAACTCCCCATCT
150 GluSerLeuAsnPheIleArgAlaHisThrProTyrIleAsnIleTyrAsnCysGluProAlaAsnProSerGluLysAsnSerProSer

631 ACCCAATACTGTTACAGCATACAATCTCTGTTCTTGGGCATTTTGTCAGTGATGCTGATCTTTGCCTTCTTCCAGGAACTTGTAATAGCT
180 ThrGlnTyrCysTyrSerIleGlnSerLeuPheLeuGlyIleLeuSerValMetLeuIlePheAlaPhePheGlnGluLeuValIleAla
            ============================================================
```

FIG. 10A-1

```
721 GGCATCGTTGAGAATGAATGGAAAAGAACGTGCTCCAGACCCAAATCTAACATAGTTCTCCTGTCAGCAGAAGAAAAAAAAGAACAGACT
210 GlyIleValGluAsnGluTrpLysArgThrCysSerArgProLysSerAsnIleValLeuLeuSerAlaGluGluLysLysGluGlnThr

811 ATTGAAATAAAAGAAGAAGTGGTTGGGCTAACTGAAACATCTTCCCAACCAAAGAATGAAGAAGACATTGAAATTATTCCAATCCAAGAA
240 IleGluIleLysGluGluValValGlyLeuThrGluThrSerSerGlnProLysAsnGluGluAspIleGluIleIleProIleGlnGlu

901 GAGGAAGAAGAAGAAACAGAGACGAACTTTCCAGAACCTCCCCAAGATCAGGAATCCTCACCAATAGAAAATGACAGCTCTCCTTAAGTG
270 GluGluGluGluGluThrGluThrAsnPheProGluProProGlnAspGlnGluSerSerProIleGluAsnAspSerSerProEnd 297
                                                                                ---CHO---

991 ATTTCTTCTGTTTTCTGTTTCCTTTTTTAAACATTAGTGTTCATAGCTTCCAAGAGACATGCTGACTTTCATTTCTTGAGGTACTCTGCA
                                                    *

1081 CATACGCACCACATCTCTATCTGGCCTTTGCATGGAGTGACCATAGCTCCTTCTCTCTTACATTGAATGTAGAGAATGTAGCCATTGTAG

1171 CAGCTTGTGTTGTCACGCTTCTTCTTTTGAGCAACTTTCTTACACTGAAGAAAGGCAGAATGAGTGCTTCAGAATGTGATTTCCTACTAA

1261 CCTGTTCCTTGGATAGGCTTTTTAGTATAGTATTTTTTTTTGTCATTTTCTCCATCAGCAACCAGGGAGACTGCACCTGATGGAAAAGAT

1351 ATATGACTGCTTCATGACATTCCTAAACTATCTTTTTTTTATTCCACATCTACGTTTTTGGTGGAGTCCCTTTTTATCATCCTTAAAACA

1441 ATGATGCAAAAGGGCTTTAGAGCACAATGGATCT 1474
```

FIG. 10A-2

FIG. 4B



```
  1 GCCCGACGAGCCATGGTTGCTGGGAGCGACGCGGGGCGGGCCCTGGGGGTCCTCAGCGTGGTCTGCCTGCTGCACTGCTTTGGTTTCATC  90
  1             MetValAlaGlySerAspAlaGlyArgAlaLeuGlyValLeuSerValValCysLeuLeuHisCysPheGlyPheIle  26

 91 AGCTGTTTTTCCCAACAAATATATGGTGTTGTGTATGGGAATGTAACTTTCCATGTACCAAGCAATGTGCCTTTAAAAGAGGTCCTATGG 180
 27 SerCysPheSerGlnGlnIleTyrGlyValValTyrGlyAsnValThrPheHisValProSerAsnValProLeuLysGluValLeuTrp  56
                                          ---CHO---

181 AAAAAACAAAAGGATAAAGTTGCAGAACTGGAAAATTCTGAATTCAGAGCTTTCTCATCTTTTAAAAATAGGGTTTATTTAGACACTGTG 270
 57 LysLysGlnLysAspLysValAlaGluLeuGluAsnSerGluPheArgAlaPheSerSerPheLysAsnArgValTyrLeuAspThrVal  86

271 TCAGGTAGCCTCACTATCTACAACTTAACATCATCAGATGAAGATGAGTATGAAATGGAATCGCCAAATATTACTGATACCATGAAGTTC 360
 87 SerGlySerLeuThrIleTyrAsnLeuThrSerSerAspGluAspGluTyrGluMetGluSerProAsnIleThrAspThrMetLysPhe 116
                          ---CHO---                                                  ---CHO---

361 TTTCTTTATGTGCTTGAGTCTCTTCCATCTCCCACACTAACTTGTGCATTGACTAATGGAAGCATTGAAGTCCAATGCATGATACCAGAG 450
117 PheLeuTyrValLeuGluSerLeuProSerProThrLeuThrCysAlaLeuThrAsnGlySerIleGluValGlnCysMetIleProGlu 146
                                                      ---CHO---

451 CATTACAACAGCCATCGAGGACTTATAATGTACTCATGGGATTGTCCTATGGAGCAATGTAAACGTAACTCAACCAGTATATATTTTAAG 540
147 HisTyrAsnSerHisArgGlyLeuIleMetTyrSerTrpAspCysProMetGluGlnCysLysArgAsnSerThrSerIleTyrPheLys 176
                                                                  ---CHO---

541 ATGGAAAATGATCTTCCACAAAAAATACAGTGTACTCTTAGCAATCCATTATTTAATACAACATCATCAATCATTTTGACAACCTGTATC 630
177 MetGluAsnAspLeuProGlnLysIleGlnCysThrLeuSerAsnProLeuPheAsnThrThrSerSerIleIleLeuThrThrCysIle 206
                                                      ---CHO---

631 CCAAGCAGCGGTCATTCAAGACACAGATATGCACTTATACCCATACCATTAGCAGTAATTACAACATGTATTGTGCTGTATATGAATGTT 720
207 ProSerSerGlyHisSerArgHisArgTyrAlaLeuIleProIleProLeuAlaValIleThrThrCysIleValLeuTyrMetAsnVal 236
                          ================================================================

721 CTTTAATTGAGAAGACAATTTCTTCATTTTTAGGTATTCTGAAATGTGACAGAAAACCAGACAGAACCAACTCCAATTGATTGGTAACAG 810
237 LeuEnd
    ===
811 AAGATGAAGACAACAGCATAACTAAATTATTTTAAAAACTAAAAAGCCATCTGATTTCTCATTT 874
```

FIG. 4A